

# Draft Genome Sequences of the *Enterococcus faecium* Strain LCT-EF258

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The space environment has been shown to affect microbes by altering various features, including morphology, growth rate, metabolism, virulence, drug resistance, and gene expression and mutation. Here we present the draft genome sequence of the *Enterococcus faecium* strain LCT-EF258, derived from the *E. faecium* strain CGMCC 1.1736, which was exposed to 17-day space flight.

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The space environment has been reported to cause biological alterations in microorganism characteristics such as growth, drug resistance, and virulence (1–4). *Enterococcus faecium* was originally defined as a group D streptococcus until DNA analysis in 1984 showed the differences in streptococci. These organisms can be part of the normal flora in human and animal intestines as well as pathogens causing nosocomial infections (1, 5). *E. faecium* is a Gram-positive bacterium belonging to the family *Enterococcaceae* (6). We employed *E. faecium* as a model to investigate the effects of space conditions on microbes. The *E. faecium* strain LCT-EF258 was derived from the strain CGMCC 1.2136, which was loaded onto the ShenZhouVIII spacecraft, which flew in space from 1 November to 17 November 2011. The whole-genome sequence of the strain LCT-EF258, which has been exposed to space flight, was determined using Illumina second-generation sequencing technology (7).

The genomic DNA of *Enterococcus faecium* LCT-EF258 was sequenced by the Illumina HiSeq2000, and shotgun sequence libraries were prepared for two types with 500 bp and 6 kb. By a series of filtering criteria, a total of 550 Mb of sequence reads was generated (read length, 90 bp). With SOAPdenovo software (8), we joined 114 contigs with a total length of 2,717,416 bp and 26 scaffolds (≥500 bp in size) with 90-kb gaps. About 190-fold coverage was achieved.

Open reading frames (ORFs) were identified with Glimmer (9), and 2,824 protein-coding sequences (CDSs) with an average gene length of 861 bp were predicted. The putative encoded proteins were compared with sequences present in public databases by using BLASTP. Other putative coding regions, either genes or pseudogenes, were identified by BLAST. tRNAs were identified by using the program tRNA-SCAN (10). rRNAs and other small RNAs were identified by BLASTN searches of the intergenic regions versus RNA-specifying genes in other published genome sequences.

The gene functional annotations were yielded by BLASTP us-

ing all predicted protein sequences, and the graphical display of the annotated genome was obtained with the KEGG (11), Clusters of Orthologous Groups (COG), Swiss-Prot, TrEMBL, Gene Ontology (GO), and NR databases. For the COG database, the genes were clustered mainly into the “carbohydrate transport and metabolism” and “general function prediction” classes. In addition, 1,901 protein families were found by comparing protein sequences with sequences in protein databases using BLASTP.

**Nucleotide sequence accession number.** The whole-genome sequence of *E. faecium* LCT-EF258 has been deposited at DDBJ/EMBL/GenBank under the accession number [ANAJ000000000](https://www.ncbi.nlm.nih.gov/nuccore/ANAJ000000000). The versions described in this paper are the first versions.

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